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October 22, 2004, 13:36:34 ; Search time 158 Seconds (without alignments) 95.358 Million cell updates/sec
                                                                                                                                                                                                                                                                      1 NOSSNFGPMKGGNFGGRSSG......GGGGQYFAKPRNQGGYGGCC 42
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                     2002273 seqs, 358729299 residues
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Gapop 10.0 , Gapext 0.5
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seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% , Listing first 45 summaries A Geneseq 23Sep04:\* Database

geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*geneseqp2002s:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Modif	Human	•	Novel	Abg04261 Novel hum	Novel	Novel	Aau29983 Novel hum	44 Human	Ade57408 Rat Prote		Aab48966 Human het		Abg00955 Novel hum	1 Mouse	Adh17083 Human hnR	Human	Novel	_	Novel	Novel	Novel	Novel	Abg15177 Novel hum	Novel
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22555555555555555555555555555555555555	ИИИИИ В В В В В В В В В В В В В В В В В	4 4 4 7

## ALIGNMENTS

Human; M9; heteronuclear ribonuclear protein type 1; hnRNP A1; NTP; nuclear targeting peptide; peptide scaffold; gene transfer; NLS; nuclear localisation signal; antiarteriosclerotic; vasotropic; gene therapy; atherosclerosis; restenosis; angioplasty. Modified M9 nuclear targeting peptide SEQ ID NO:1. AAY82221 standard; peptide; 42 AA. (first entry) 13-JUN-2000 AAY82221; RESULT 1 AAY82221 

WO200012114-A1. Homo sapiens. 09-MAR-2000.

99WO-US020122. 98US-0098791P. 01-SEP-1999; 01-SEP-1998;

(UYPE-) UNIV PENNSYLVANIA.

Diamond SL;

WPI; 2000-256490/22.

Delivering molecules to nuclei of eukaryotic cells for use in gene transfer methods uses a nuclear targeting peptide which contains a nonclassical nuclear localization signal.

Claim 8; Page 17; 40pp; English.

The present invention describes a composition for enhancing delivery of a molecule to the nucleus of eukaryotic cells, comprising a nuclear trageting peptide (MTP) containing a non-classical nuclear localisation signal (NLG). The composition can have antiarteriosclerotic and vasotropic activities, and can be used in gene therapy. The composition set is used to treat a patient having a condition associated with lack of expression of a selected nucleic acid sequence. The compositions are particularly useful for arterial gene transfer, to treat atherosclerosis and restenosis following angioplasty. The present sequence represents a specifically claimed NTP which comprises the human heteronuclear ribonuclear protein type 1 (hnRNP A1) M9 epitope with a carboxy terminal

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Gaps

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cysteine residue

Sequence 42 AA;

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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABD54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens in polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertinity, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and vaginitis), immune disorders (e.g., congenital and acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                Human, ovarian antigen, ovary, ovarian, breast, cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; disorder; anovulation; polycystic ovary syndrome; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
100.0%; Score 243; DB 3; Length 42; 100.0%; Pred. No. 6.5e-21; ive 0; Mismatches 0; Indels
                                                                                                                           1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGGGC 42
                                                                                   1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNOGGYGGGC
                                                                                                                                                                                                                                                                                                                                                            Human ovarian antigen HOCQM24, SEQ ID NO:3605.
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                                                                                                                                                                                                                                 ABP42473 standard; protein; 76 AA
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                                                                                                                                                                                                                                                                                                                    22-AUG-2002 (first entry)
                                        Conservative
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               Local Similarity
tes 42; Conserv
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  Query Match
                                          Matches
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immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders (e.g., anaemia), cardiovascular disorders, and utinary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may luther be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 40; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #3360.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                Sequence 76 AA;
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polypeptide and polynucleotide sequences have applications in polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent movel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invention.

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Gaps

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40

93.8%; Score 228; DB 4; Length 296; 100.0%; Pred. No. 2.5e-18; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100.\* Matches 40; Conservative

Sequence 296 AA;

244 NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 283

1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders
supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent movel human diagnostic patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                  198 NQSSNFGPMKGGNFGRSSGPYGGGGQYFAKPRNQGGYGG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #9546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG09555 standard; protein; 296 AA
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                             Sequence 250 AA;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain areaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                               Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             claim 20; SEQ ID NO 34620; 103pp; English.
                                                                                                                               Novel human diagnostic protein #4252.
               ABG04261 standard; protein; 296 AA.
                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
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                                                                                         (first entry)
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N-PSDB; AAS68448.
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ABG0426
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG310377 represent novel human diagnostic panen acid sequences of the invention. Note: The sequence data for this parent din not appear in the printed specification, but was obtained in electronic format directly from WIPO at the type. Wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                 Length 296;
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                                                                                                                                                                                                                         244 NOSSNFGPMKGGNFGRSSGPYGGGGQYFAKPRNQGGYGG 283
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100.0%; Pred. No. 2.5e-18;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                ABG03366 standard; protein; 296 AA
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23-AUG-2000; 2000US-00649167.
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N-PSDB; AAS67553.
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                                                                                                                                            Query Match
Best Local Similarity
Matches 40; Conserv
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                                                                                                                        Sequence 296 AA;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polynucleotides are also used and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations diagnostics for generative solutions to their traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Abg000010-Abg30377 represent novel human diagnostic
                                                                                                                                                                                                                      ö
and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at electronic format directly from WIPO at the type.int/pub/published_pct_sequences
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                      ;
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                                                                                                                                                                                 Length 296;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                244 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
                                                                                                                                                                                                                                                             1 NOSSNFGPMKGGNFGGRSSGPYGGGGGYFAKPRNQGGYGG
                                                                                                                                                                               93.8%; Score 228; DB 4; 1 100.0%; Pred. No. 2.5e-18;
                                                                                                                                                                                             100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 45535; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #15167.
                                                                                                                                                                                                                                                                                                                                                                                                 ABG15176 standard; protein; 296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-00540217.
2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8-FEB-2002 (first entry)
                                                                                                                                                            Query Match
Best Local Similarity 100..
Lag 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS79363
                                                                                                                                            Sequence 296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG15176;
                                                                                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                              ABG15176
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypunclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity

Claim 20; SEQ ID NO 33725; 103pp; English

0;

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Indels

Pred. No. 2.5e-18; Mismatches 0;

100.001 14 (\$0.001

Best Local Similarity 100. Matches 40; Conservative

244 NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG

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0;

Gaps ..

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells corpressing the proteins are useful for identifying a therapeutic agent corpressing the polypeptide. We to respression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used to express them are also useful for producing the proteins. The proteins and/or nerve tissue growth or regeneration; immune suppression and/or and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU39510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
amino acid sequences of the invention. Note: The sequence data for th patent did not appear in the printed specification, but was obtained electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                          Query Match 93.8%; Score 228; DB 4; Length 296; Best Local Similarity 100.0%; Pred. No. 2.5e-18; Matches 40; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 NQSSNFGPMKGGNFGRSSGPYGGGGQYFAKPRNQGGYGG 283
                                                                                                                                                                                                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                                                                                                                                                                    1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU29983 standard; protein; 296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted protein #474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-2001; 2001WO-US008656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 296 AA;
                                                                                                                                                                                              Sequence 296 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU29983;
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AAU29
AAU39
AAU
       8X33333
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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalogathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERAP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                 Huntington's disease; osteoarthritis; Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; expodence epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
                                                                                                                                            Human heat mitochondrial protein as a therapeutic target SeqID1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĞM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 228; DB 7; Length 298;
Pred. No. 2.5e-18;
                                                                                                                                                                             mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibson BW, Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1550; 180pp; English.
                                     Ę.
                                     ADJ69744 standard; protein; 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-2003; 2003WO-US010870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MITO-) MITOKOR.
(BUCK-) BUCK INST AGE RES.
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fahy ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-845369/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with the disease
                                                                                                                                                                                                                                                                                                                                                                     WO2003087768-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 298
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                             06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shosh SS,
Warnock DE;
RESULT 9
ADJ69744
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DB 4; Length 296;

93.8%; Score 228;

0

Gaps

0;

40;

Matches

Db

ADE57408;

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The present sequence represents the human heterogeneous nuclear ribonucleoprotein (hnRNP) core protein A1, which is used to exemplify the method of the present invention. The hnRNP A1 gene can be found on the genbank database accession number X12671, NID 932344. The present invention describes a method for the detection of a protein coding region in a DNA base sequence by judging the probability where a specific sequence will be found. The method comprises utilizing the appearance frequency in the coding and the noncoding regions. The method allows noise in the noncoding region to be reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, heterogeneous nuclear ribonucleoprotein; core protein; hnRNP; RNA binding protein; detection; coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of protein code region on DNA base sequence - using method which reduces interference from noncoding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human heterogeneous nuclear ribonucleoprotein core protein Al
                                                           Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 320;
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                          267 NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 306
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                                                                                                                                                              1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
                                                     Score 228; DB 7; Pred. No. 2.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.8%; Score 228; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 40; Conservative 0; Mismatches 0;
                                       93.8%; Scc...
100.0%; Pred. No. 2...
'-- 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  AAW55828 standard; protein; 320 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96JP-00179521.
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                               Query Match
Best Local Similarity 100.0
Them 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HITA ) HITACHI LTD
     Sequence 319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV25978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 320 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                     AAW55828;
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                                                                                                                                                                                                                                                                                             RESULT 11
AAW55828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially required in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that increases or decreases the increase or decreases the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition or small molecule that regulates the activity of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating method for their an endoment for properties or the repulse of the polypeptides or their antibodies. The polymelectication or more of the polypeptides or their antibodies. The polymelectication or more of the polypeptide or the composition comprising the one or more polypeptides or their antibodies. The polymelectication or more or m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
  Gaps
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Indels
                                                                                       246 NQSSNFGPMKGGNFGRSSGPYGGGGQYFAKPRNQGGYGG 285
                                                     40
                                                     1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
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  0; Mismatches
                                                                                                                                                                                                                                    ADE57408 standard; protein; 319 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                            29-JAN-2004 (first entry)
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-268312/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus.
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Woolf C,

27-FEB-2003

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Gaps

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This sequence represents human heterogeneous nuclear ribonucleoprotein Al (hnRNP Al). hnRNP Al (also known as heterogeneous nuclear ribonucleoprotein core protein Al and pade AporRs) is thought to function in the stabilisation, transport and processing (including alternative the stabilisation, transport and processing (including alternative splicing) of newly synthesised mRNAs. It facilitates the annealing of single-stranded nucleic acids, modulates the binding of single-stranded nucleic acids, modulates the binding of single-stranded nucleic and shuttles continuously between the nucleus and the intron sequences, and shuttles continuously between the nucleus and the cytoplasm acting as a carrier protein for mRNAs. hnRNP Al also participates in telomere biogenesis, with low lavels of hnRNP correlating with shortened telomeres. In addition, hnRNP Al has also been classified as an apoptosis-associated protein on the basis that it is specifically clasvillity to control splicing events, particularly donor splice site selection, hnRNP Al is implicated in the process of oncogenesis. The invention relates to antisense oligonucleotides targetted to the hnRNP Al mrNA, and were analysed for their effect on hnRNP Al mRNA, and were analysed for their effect on hnRNP Al mRNA, and were analysed for their effect on hnRNP Al mRNA, and were analysed for their effect on hnRNP Al mRNA, and were analysed for their effect on hnRNP Al mRNA and were analysed for their effect on hnRNP Al mRNA and were analysed for their effect on hnRNP Al mRNA and were analysed for their effect on hnRNP Al mRNA and were analysed for their effect on hnRNP Al mRNA and were analysed for their effect on hnRNP Al mRNA and were analysed for their effect on hnRNP Al mRNA and were analysed for their effect on hnRNP Al mRNA and were analysed for their effect on hnRNP Al mRNA and were analysed for their effect on hnRNP Al mRNA is evels with hnRNA all expension, such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel antisense compound targeted to human hnRNP A1 which specifically hybridizes with and inhibits the expression of human hnRNP A1, useful for modulating the expression of hnRNP A1 in cells.
                                                                     heterogeneous nuclear ribonucleoprotein core protein Al; p40cRs; mRNA processing; transport; stabilisation; alternative splicing; donor splice site selection; telomere biogenesis; oncogenesis; apoptosis-associated protein; cancer; tumour formation; expression inhibition; antisense therapy.
Human heterogeneous nuclear ribonucleoprotein Al (hnRNP Al).
                                                      Human hnRNP A1; heterogeneous nuclear ribonucleoprotein A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 16; Col 43-48; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         99US-00428696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00428696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-090484/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC92731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         27-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-1999;
                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                 US6165789-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                               Gaps
                               ;
0
   Length 320;
                              0; Indels
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                                                            1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
93.8%; Score 228; DB 4; I
100.0%; Pred. No. 2.7e-18;
tive 0; Mismatches 0;
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268 NOSSNFGPMKGGNFGRSSGPYGGGGQYFAKPRNQGGYGG 307
                                                          AAB81934 standard; protein; 320
                                                                              AAB81934;
                                        RESULT 13
                                               AABB1934
ID AAB
XX
AC AAB
XX
DT 25-
    g
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(first entry)

25-JUN-2001

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Marmoset, vitamin D response element binding protein, VDRE-BP, lymphoma, vitamin D resistance, osteoporosis, hypercalcaemia; vitamin D toxicity, glucocorticoid mediated disorder, granuloma forming disease; vitamin D intoxication; steroid hormone hypersecretion; gene therapy.
Marmoset vitamin D response element binding protein #1.
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Saguinus oedipus.

WO200121649-A2.

29-MAR-2001

20-SEP-2000; 2000WO-US025844.

99US-00400967.

22-SEP-1999;

(CEDA-) CEDARS SINAI MEDICAL CENT.

Adams JS;

WPI; 2001-308082/32 N-PSDB; AAF85636.

in New vitamin D response element-binding protein (VDRE-BP) useful in modifying vitamin D receptor activity, in producing anti-VDRE-BP antibodies, in identifying agonists and antagonists of the protein, or

Claim 17; Page 71-72; 81pp; English.

gene therapy.

The present invention provides the protein and coding sequences for two vitamin D response element binding proteins (VDRE-BPS) from the marmoset. These confer vitamin D resistance on the primate, a characteristic which is associated with high circulating levels of other steroid hormones. The sequences provided by the invention can be used to identify treatments for osteoproses, hypercalcaemia, vitamin D intoxication, steroid hormone hypersecretion, glucocorticoid mediated disorders, lymphoma and granuloma forming diseases. The present sequence is one of the VDRE-BPS of the Invention

Sequence 320 AA;

Gaps · 0 Length 320; Score 228; DB 4; Pred. No. 2.7e-18; 93.8%; Scor. 100.0%; Pred. No. 2... 0; Mismatches 40; Conservative Query Match Best Local Similarity Matches

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40 268 NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG

> à Db

ABG00955 standard; protein; 320 AA

ABG0095

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                    Novel human diagnostic protein #946.
                                                                                                                                                      30-MAR-2001; 2001WO-US008631.
                                  (first entry)
                                                                                                                   WO200175067-A2
                                                                                                  Homo sapiens
                                  13-FEB-2002
                                                                                                                                      11-OCT-2001.
```

Tang YT;

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed serivity of in a useful in gene therspy techniques to restore normal ectivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations copypaptide and polynuclectide sequences have applications in diagnostics for generatic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic manno acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification.
                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 31314; 103pp; English
  31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                 WPI; 2001-639362/73.
N-PSDB; AAS65142.
                                                                             (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 320 AA;
                                                                                                                                                                                                                                                                                                                                            biodiversity.
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Gaps . 0 Length 320; 0; Indels 1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 40 93.8%; Score 228; DB 4; I 100.0%; Pred. No. 2.7e-18; iive 0; Mismatches 0; Query Match
Best Local Similarity luv..
Anna 40; Conservative à

0

268 NQSSNFGPMKGGNFGRSSGPYGGGGOYFAKPRNQGGYGG 307

ABB57241 standard; protein; 320 AA

ABB57241;

(first entry) 07-MAR-2002

Mouse, ischaemia, compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition, ischaemic disease.

Mouse ischaemic condition related protein sequence SEQ ID NO:645.

Mus musculus.

WO200188188-A2.

22-NOV-2001

18-MAY-2001; 2001WO-JP004192.

18-MAY-2000; 2000JP-00145977. RESULT 15
ABB57241
ID ABB572
XX
AC ABB572
XX
DT 07-MAE
XX
KW Mouse;
KW Vasosg
XX
XX
COS Mus m
CO

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemia condition (e.g. compressive ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB7020 to ABB57374) or by determining the protein sequences in ABB7020 to ABB57374) or by determining the protein profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these Ishii Y; Takahashi Y, Nagata T, (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON Claim 2; Page 1623-1625; 2690pp; English Ishikawa K, Asai S, WPI; 2002-034733/04. N-PSDB; ABI99624 Sequence 320 AA; geneg 

., Length 320; Indels / Match 93.8%; Score 228; DB 5; L Local Similarity 100.0%; Pred. No. 2.7e-18; Pse 40; Conservative 0; Mismatches 0; Query Match Best Loca Matches

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Gaps

1 NQSSNFGPMKGGNFGGRSGPYGGGQQYFAKPRNQGGYGG 40 à 셤

completed: October 22, 2004, 13:43:04 is: 161 secs Search cor Job time

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

October 22, 2004, 13:40:25; Search time 37 Seconds (without alignments) 109.219 Million cell updates/sec Run on:

US-09-763-982B-1

243 1 NQSSNFGPMKGGNFGGRSSG......GGGGQYFAKPRNQGGYGGGC 42 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

seg length: 0 seg length: 200000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SITMMARIES

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glycine-rich prote	RNA-binding protei	ATP-dependent RNA	probable ATP-depen	glycine-rich RNA-b	probable glycine r	hypothetical prote	conserved hypothet	keratin 10, type I	glycine-rich RNA b	snRNP-associated p	hypothetical prote	glycine-rich prote	glycine-rich RNA-b	glycine-rich prote	glycine-rich prote
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169	334	604	633	161	175	290	341	593	145	386	1585	82	142	157	155
34.0	34.0	34.0	34.0	33.7	33.7	33.5	33.5	33.5	33.3	33.3	33.3	33.1	33.1	33.1	32.9
82.5	82.5	82.5	82.5	8	82	81.5	81.5	81.5	81	81	81	80.5	80.5	80.5	80
0		32	m	4	ري ري	36	7	38	39	0	-	2	m	44	м

## ALIGNMENTS

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Duracterate names: single-stranded DNA-binding protein
C)Species: Ratus norvegicus (Norway rat)
C)Baceles: Ratus norvegicus (Norway rat)
C)Bacelesion: A02682
R)Cobianchi, F.; Sendupta, D.N.; Zmudzka, B.Z.; Wilson, S.H.
J. Biol. Chem. 261, 3536-3543, 1986
A)Tille: Structure of rodent helix-destabilizing protein revealed by cDNA cloning.
A)Reference number: A02682; MUID:86140140; PMID:3005291
A)Recession: A02682
A)Accession: A02682
A)Accession: A02682
A)Accession A02682
C)Comment: This protein was isolated from the brain.
C)Comment: This protein repeat homology <a href="Right">Reference the protein repeat homology <a href="Right">Right (Right) #Right (Right) #Right (Right) #Right) #Right (Right) #Right (Right) #Right (Right) #Right (Right)
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heterogeneous ribonuclear particle protein Al - mouse
NyAlternate names: helix-destabilizing protein; hnRNP core protein Al; single stranded DN (Species: Mus musculus (Rouse mouse)
C;Species: Mus musculus (Rouse mouse)
C;Accession: A44485; JC5070; JC5071
R;Ben-David, Y; Bani, M.R; Chabot, B.; De Koven, A.; Bernstein, A.
MOI. Cell. Biol: 12, 4449-4455, 1992
A;Title: Retroviral insertions downstream of the heterogeneous nuclear ribonucleoprotein A;Reference number: A44485; MUID:93024387; PMID:1406633
A;Accession: A44485
A;Molecule type: mRNA
A;Residues: 1-320 ABEN>
A;Reference extracted from NCBI backbone (NCBIP:114165)
A;Ritle: Nolecular cloning of the genes suppressed in RVC lymphoma cells by topoisomerase
A;Reference number: JC5070; MUID:97069646; PMID:8912629

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Gaps

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A;Introns: 5/3; 44/3; 93/3; 164/1; 195/1; 226/1; 251/1; 303/1
C;Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology
C;Keywords: acetylated amino end; alternative splicing; DNA binding; duplication; methyle
F;15-81/Domain: ribonucleoprotein repeat homology <RRML>
F;16-172/Domain: ribonucleoprotein repeat homology <RRML>
F;16-172/Jomain: ribonucleoprotein repeat homology </ri>
F;16-172/Jomain: ribonucleoprotein rep
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Cross-references: UNIPROT: P09651; EMBL: X06747; NID: g36101; PIDN: CAA29922.1; PID: g36102
C; Keywords: acetylated amino end; alternative splicing; DNA binding; methylated amino aci
F; F; F5-81/Domain: ribonucleoprotein repeat homology RRM1>
F; D0-172/Domain: ribonucleoprotein repeat homology ARM1>
F; 106-172/Domain: ribonucleoprotein repeat homology ARM2>
F; 2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F; 194/Modified site: omega-N, omega-N-dimethylarghnine (Arg) #status predicted
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Bjochim. Blophys. Acta 1172, 292-300, 1993
A;Title: CDNA cloning of a hnRNP A1 isoform and its regulation by retinol in monkey tract
A;Reference number: S30192; WUID:93192320; PMID:8448206
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A,Aolecule type: mRNA
A,Residues: 1-320 cangs
A,Cross-references: UNIPROT:028521; EMBL:M84334; NID:g1339834; PIDN:AAB01436.1; PID:g1332
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A,Molecule type: mRNA
A,Residues: 'IC',3.3.20
A,Cross-references: EMBL:M84334
C;Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology
C;Reywords: acetylated amino end; methylated amino acid
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NALternate names: heterogeneous nuclear ribonucleoprotein Al; hnRNP Al
C;Species: Macaca mulatta (Thesus macaque)
C;Species: May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                            Length 320;
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                                                                                                                                                                                                                                                                                                                                        Query Match 93.8%; Score 228; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 40; Conservative 0; Mismatches 0;
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submitted to the EMBL Data Library, February 1992
A;Reference number: S34126
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Matches 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C_Comment: This protein inhibits the activity of the SF2/SAF factor in regulating the sp_C_Comment: This protein inhibits the activity of the SF2/SAF factor in regulating the sp_C_SUBPATEMAILY: Helix-destabilizing protein, ribonucleoprotein repeat homology (RRM1) actevlated amino end; alternative splicing; DNA binding; duplication; methyl F;15-81/Domain: ribonucleoprotein repeat homology (RRM1)  
F;106-172/Domain: ribonucleoprotein repeat homology (RRM2)  
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted F;194/Modified site: omega-N,omega-N-dimethylarginine (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                 A; Cross-references: DDBJ:D86729; NID:g1711241; PIDN:BAA13162.1; PID:g1711242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%; Score 228; DB 1; L
100.0%; Pred. No. 1.6e-17;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N,Alternate names: hnRNP core protein Al N,Contains: helix-destabilizing protein UP1
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A;Gene: GDB:HNRPA1
A;Crose-references: GDB:127388; OMIM:164017
A;Map position: 12q13-12q13
                                                                                                                                                                                                                           A Molecule type: mRNA
A,Residues: 1-251,279-320 <0N2>
A)Cross-references: DDBJ:D86728
A;Experimental source: lymphoma cell
                                                                                                                                                            A; Experimental source: lymphoma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 40; Conservative
                                              A; Molecule type: mRNA
A; Residues: 1-320 <ONI>
           A, Accession: JC5070
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CyAccesion: S4078
RyGood, P.U.; Rebbert, M.L.; Dawid, I.B.
Nucleic Acids Res. 21, 999-1006, 1993
A;Attle: Three new members of the RNP protein family in Xenopus.
A;Accession: S40779
A;Accession: S40779
A;Accession: 1-385 CGOOs
A;Accession: 1-38
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B34504

B4504

B4604

B54504

B54504

B54504

B54504

B54504

B54504

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B5500

B5500
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A, Cross-references: EMBL: L02956; NID: 2214744; PIDN: AAA49949.1; PID: G214745
C, Superfamily: helix-destabilizing protein, ribonucleoprotein repeat homology
E, 28-94/Domain: ribonucleoprotein repeat homology <RRML>
F, 119-185/Domain: ribonucleoprotein repeat homology <RRML>
                               heterogeneous ribonuclear particle protein A3 - African clawed frog N; Alternate names: heterogeneous nuclear ribonucleoprotein A3 C; Species: Stenopus laevis (African clawed frog) C; Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004 C; Accession: $40777; $41738 R; God, P.J.; Rebbert, M.L.; Dawid, I.B. Nucleic Acids Res. 21, 999-1006, 1993 Nucleic Acids Res. 21, 999-1006, 1993 A; Fitle: Three new members of the RNP protein family in Xenopus. A; Reference number: $40774; MUID:93197168; PMID:8451200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 385;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GGRSSGPYGGGGQYFAKPRNQGGYGG
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Pred. No. 3.4e-05;
2; Mismatches 10; Indels
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Pred. No. 1.4e-05;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P51968; EMBL:L02956
RR;Good, P.-G.; Lai, M.; Rebbert, M.L.; Dawid, I.B.
submitted to the EMBL Data Library, October 1992
A;Reference number: S41738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
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nilarity 55.6%;
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Best Local Similarity 52.1%;
Matches 25; Conservative
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les 25; Conserv
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Matches
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A; Residues: 1-365 < KAY>
A; Cross-references: UNIPROT: P17130; GB: M31041; NID: G214238; PIDN: AAA49741.1; PID: G214239
C; Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology
C; Keywords: alternative splicing; DNA binding; duplication; nucleus
F;15-81/Domain: ribonucleoprotein repeat homology < RRMI>
F;106-172/Domain: ribonucleoprotein repeat homology < RRMI>
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C.Superfamily: helix destabilizing protein; ribonucleoprotein repeat homology
F;10-76/Domain: ribonucleoprotein repeat homology <RRM1>
F;101-167/Domain: ribonucleoprotein repeat homology <RRM2>
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A4840

At 4840

Nivalternate names: heterogeneous nuclear ribonucleoprotein Xala

Gispeciaes: Xenopus laevis (African clawed frog)

Gispeciaes: Xenopus laevis (African clawed frog)

Giste: 13-011-1990 #sequence_revision 13-011-1990 #text_change 09-011-2004

Giste: 13-011-1990 #sequence_revision 13-011-1990 #text_change 09-011-2004

Riffay, B.K.; Sawhney, R.K.; Wilson, S.H.

Riffay, B.K.; Sawhney, R.K.; Wilson, S.H.

Aitle: Potential for two isoforms of the Al ribonucleoprotein in Xenopus laevis.

Aitle reach number: A34840

Aitherance number: A34840

Aitherance number: A34840

Aitherance number: A34840

Aitherance number: A34840
F;15-81/Domain: ribonucleoprotein repeat homology <RRM1>
F;106-172/Domain: ribonucleoprotein repeat homology <RRM5>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F;194/Modified site: omega-N.omega-N-dimethylarginine (Arg) #status predicted
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840775
C. Species  
Sandy  
C. Species  
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Pred. No. 3.7e-06;
1; Mismatches 9; Indels
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Pred. No. 1.4e-06;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SSNFGPMKGGNF-GGRSSGPYGG--GGQYFAKPRNQGGYGGG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 NOSSNFGPMKGGNFGGRSLGPYGGGGQYFAKPRNQGGYGG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
                                                                                                                                                                                                                                                                                             Score 222; DB 2;
Pred. No. 7e-17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.3%;
64.3%;
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Best Local Similarity 64.4%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.5%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Conservative
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Query Match Best Local Similarity

ò g

5

5

298

4

Gaps

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A; Cross-references: UNIPROT.P51990; EMBL:L02955; NID:g214742; PIDN:AAB59951.1; PID:g21474
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C;Superfamily: helix-destabilizing proterin; ribonucleoprotein repeat homology
F;10-76/Domain: ribonucleoprotein repeat homology <RRML>
F;101-167/Domain: ribonucleoprotein repeat homology <RRML>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine-rich RNA-binding protein - rape (5,8pecies: Brassica napus (rape) (5,8pecies: Brassica napus (rape) (5,8pecies: Brassica napus (rape) (5,8pecies: Brassica napus (rape) (5,8cecssion: 838331; 825120 (5,8cecssion: 838331; 825120 (6,8cecssion: 838331; 825120 (7,8cecssion: 838331; 825120 (7,8cecssion: 81040)% Acta 1216, 123-125, 133-125, 138-185 (6,8cecssion: 81040)% Acta 1216, 123-125, 138-185 (6,8cecssion: 81040)% Acta 1216, 123-125, 159-18642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P17130; GB:M30575; NID:g214240; PIDN:AAA49742.1; PID:g214241 C;Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology C;Keywords: alternative splicing; DNA binding; duplication; nucleus F;15-81/Domain: ribonucleoprotein repeat homology <RRM1> F;16-172/Domain: ribonucleoprotein repeat homology <RRM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: Q05966; EMBL: Z14143; NID: 917818; PIDN: CAA78513.1; PID: 917819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: B34840
R;Kay, B.K.; Sawhney, R.K.; Wilson, S.H.
Rpcc, Natl. Acad. Sci. U.S.A. 87, 1367-1371, 1990
A;Title: Potential for two isoforms of the Al ribonucleoprotein in Xenopus laevis. A;Reference number: A34840; MUID:90160329; PMID:2137612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
F;7-74/Domain: ribonucleoprotein repeat homology <RRM1>
R;Good, P.J.; Rebbert, M.L.; Dawid, I.B.

Nucleic Acids Res. 21, 999-1006, 1993
A;Title: Three new members of the RNP protein family in Xenopus.
A;Reference number: S40774; MUID:93197168; PMID:8451200
A;Accession: S40776
A;Accusion: S40776
A;Reference not shown; translation not shown
A;Residues: 1-358 <GOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: heterogeneous nuclear ribonucleoprotein XAlb
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heterogeneous ribonuclear particle protein Al.b - African clawed frog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 QSSNFGPMK-GGNFGGRSS--GPYGGGGQYFAKPRN-----QGGYGG
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44.4%; Score 108; DB 2; L
Best Local Similarity 56.2%; Pred. No. 0.00016;
Matches 27; Conservative 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.2%; Score 107.5; DB 2;
87.0%; Pred. No. 0.00017;
ative 2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-351 < KAY>
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A;Residues: 1-169 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S38331
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Best Local (
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                                                        A;Title: Structure and expression of the gene (HNRPA2B1) encoding the human hnRNP protei
A;Reference number: A56845; MUID:95309902; PMID:7789969
A;Accession: A56845
                                                                                                                                                                  A;Status: mucleic acid sequence not shown
A;Molecule type: DNA
A;Cross-references: UNIPROT: P22626; GB:D28877; NID:G565642; PIDN:BAA06031.1; PID:G565643
R;Burd, C.G.; Swanson, M.S.; Goerlach, M.; Dreyfuss, G.
A;Molecule Solid Molecule SNA
A;Title: Primary structures of the heterogeneous nuclear ribonucleoprotein A2, B1, and CA;Reference number: A34504; MUID:90099350; PMID:2557628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A34504
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2.15-353 <BB.M29064
A;Cross-references: GB.M29064
A;Cross-references: GB.M29064
A;Cross-references: CB.M29064
A;Cross-references: CB.M29064
A;Cross-references: CB.M29064
A;Cross-references: CB.M29062, 1994
A;Title: Two homologous genes, originated by duplication, encode the human hnRNP protein
A;Reference number: S48057; MUID:94301779; PMID:8029005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Note: this protein was shown to be ADP-ribosylated
R.Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; C
Blectrophoresis 11, 528-536, 198
A;Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencin
A;Reference number: A61002; MUD:91031404; PMID:1699755
A;Accession: E61013
A;Accession: E61013
A;Residues: 63-69;204-212;214-220,'F', 221-228 <BAU>
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A/Cross-references: GDB-377778; OMIM:600124
A/Map position: 7p15-7p15 / 100/3; 171/1; 205/1; 232/1; 253/1; 293/1; 334/1
A/Introns: 2/3; 14/3; 51/3; 100/3; 171/1; 205/1; 232/1; 253/1; 293/1; 334/1
C/Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology C/Keywords: alternative splicing; duplication; nucleus; RNA binding C/Keywords: alternative splicing; duplication; nucleus; RNA binding F;12.15-35/Domain: heterogeneous ribonuclear particle protein A2 <HA2> F;22-88/Domain: ribonucleoprotein repeat homology <RRM1> F;113-179/Domain: ribonucleoprotein repeat homology <RRM2>
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A;Title: App-ribosylation of heterogeneous ribonucleoproteins in Hela cells. A;Reference number: PC2221; MUID:95071393; PMID:7980541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribonucleoprotein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S40776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A,Cross-references: GB:M29064; NID:g337452; PIDN:AAA60271.1; PID:g337453
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56.1%; Pred. No. 3.5e-05;
tive 1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 OPSNYGPMKSGNFGGSRNMGGPYGGGNYGPGGSGGGGG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: protein
A,Residues: 'XXX',83-86,'X',88-93,'X',95-100 <PRA>
A,Experimental source: HeLa cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary
A,Moleoule type: DNA
Residues: 1-353 ABIA>
A,Cross_references: EMBL:U09122
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Best Local Similarity 56.1
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: B34504
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ä

Gaps

C; Genetics:

DB 1; Length 169;

39.9%; Score 97;

Query Match

RESULT 11

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91ycine-rich RNA-binding protein - rice

91ycine-rich RNA-binding protein - rice

C;Species: Oryza sativa (rice)

C;Species: Oryza sativa (rice)

C;Date: 24-Nar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C;Accession: T03583

R;Lee, M.C.; Kim, C.S.; Yi, B.Y.; Lee, J.S.; Eun, M.Y.

Submitted to the EMBL Data Library, June 1997

A;Description: Isolation and characterization of RNA-binding glycine rich protein of rich

A;Reference number: Z14958

A;Reference number: Z14958

A;Reference number: Z14958

A;Residue: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-165 <- LES - A;Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:Q99070, EMBL:X57662, NID:g21624, PIDN:CAA40862.1; PID:g21624, A;Note: in the authors' translation two additional Gly are shown after 110-Gly A,Note: in the authors' translation two additional Gly are shown after 110-Gly C,Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology C;Reywords: GTP binding F;9-76/Domain: ribonucleoprotein repeat homology <RRM1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycine-rich RNA-binding protein (clone S2) - sorghum
C;Species: Sorghum bicolor (sorghum)
C;Species: Sorghum bicolor (sorghum)
C;Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change. 09-Jul-2004
C;Accession: S12312
R;Cretin, C; Puigdomenech, P.
Plant Mol. Biol. 15, 783-785, 1990
A;Title: Glycine-rich RNA-binding proteins from Sorghum vulgare.
A;Reference number: S12311; MUID:91346715; PMID:1715211
A;Accession: S12312.
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38.5%; Score 93.5; DB 1; Length 168;
Best Local Similarity 56.2%; Pred. No. 0.0028;
Matches 18; Conservative 2; Mismatches 11; Indels
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Best Local Similarity 58.1%; Pred. No. 0.0066;
Matches 18; Conservative 2; Mismatches 9; Indels
                                                  Indels
Best Local Similarity 51.4%; Pred. No. 0.0012;
Matches 18; Conservative 2; Mismatches 15;
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Job time : 38 secs
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A; Residues: 1-168 < CRE>
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October 22, 2004, 13:37:19; Search time 194 Seconds (without alignments) 124.566 Million cell updates/sec
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                                                                                             1 NOSSNFGPMKGGNFGGRSSG......GGGGQYFAKPRNQGGYGGGC 42
                                                                                                                                                                                                                                                                                                                Description
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                   1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROAL XENLA
Q6IP29
AAH72090
                                                                                                                                                                                                                                                                                                                             Q9BSM5
Q6P6G9
AAH62235
ROA1_MOUSE
ROA1_RAT
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AAH33714
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ROA1 HUMAN
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ROA3 HUMAN
AAQ63629
ROA3 RAT
AAQ63630
AAH64824
AAH64824
RO21 XENLA
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Maximum Match 100%
Listing first 45 summaries
                               OM protein - protein search, using sw model
                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                       UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
                                                                             US-09-763-982B-1
243
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Match Length
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Perfect score:
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Q6nyw8 brachydanio Aah66434 brachydan Q7zw4 kenopus lae P51968 xenopus lae P51962 xenopus lae G6pcv9 mus musculu Aah59107 mus musculu Q86260 mus musculu Q81279 mus musculu Q91279 mus musculu Q91279 mus musculu Q91373 mus musculu Q91373 mus musculu Q803X3 brachydanio	Buteleostomi; Homo. sees. sees. gth 298;	e) a; Euteleostomi; e; Murinae; Rattus. e J.G.,
32 117 48.1 314 2 Q6NVW8 33 117 48.1 314 2 AAH66434 34 117 48.1 314 2 AAH66434 35 116 47.1 346 2 Q7ZWV4 36 114.5 47.1 385 1 RO31_XENLA 37 114 46.9 219 2 Q6CZAO 40 114 46.9 341 1 ROA2_MOUSE 41 114 46.9 341 2 Q91ZW9 43 114 46.9 353 1 ROAZ_HUWAN 44 112.5 46.3 422 2 Q80ZW71	PRELIMINARY; PRT; 298 AA.  101 (TrEMBLrel. 17, Created)  104 (TrEMBLrel. 26, last annotation update)  105 (TrEMBLrel. 26, last annotation update)  106 (TrEMBLrel. 26, last annotation update)  107 (TrEMBLrel. 26, last annotation update)  108 (TrEMBLrel. 26, last annotation update)  108 (TremBlrel. 26, last annotation update)  109 (TremBlrel. 26, last annotation update)  100 (TremBlrel. 26, last annotation update)  109 (TremBlrel. 26, last annotation update)  100 (TremBlrel. 26, last annotation update)	40; CORSELVATIVE 0; MISMACLNES  1 NGSSNFGPMKGGNFGRSSGPVGGGGYFAKPRNGGG 246 NGSSNFCPMKGGNFGRSSGPVGGGGYFAKPRNGGG 246 NGSSNFCPMKGGNFGRSSGPVGGGGYFAKPRNGGG 1D-2004 (TrEMBLrel. 27, Last sequence upda 1D-2004 (TrEMBLrel. 27, Last sequence upda 1D-2004 (TrEMBLrel. 27, Last annotation upper norvegicus (Rat).  10 protein.  10 protein.  11 protein.  12 protein.  13 AA.  13 AA.  11

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MEDLINE=2298257; PubMed=12477932;

Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.L., Wang J.,

Brownstein M.J., Usdin T.B., Torshyuki S., Carnino I.,

Brownstein M.J., Usdin T.B., Torshyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards. S., Worley D.M., Sodroia A.M., Gay L.J., Hollyk S.W.,

A Villalon D.K., Muzny D.M., Sarcia A.M., Gabbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mithing M., Madan A., Young A.C., Shevchenky Y., Bouffard G.G.,

Mithing M., Madan A., Young A.C., Shevchenky Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schuttz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH62235 PRELIMINARY; PRT; 313 AA.
AAH62235;
O2-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hnrpal protein.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     Strausberg R., Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM RNP 1; UNKNOWN 2.
SEQUENCE 313 AA; 33620 WW; AE0EECI0972DEF7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 300
                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC062235, AAH62235.1; -...
InterPro; IPR000564; RNA_rec_mot.
PFono, PF00076; RRM_1; 2.
SMART; SM00360; RRM; 2.
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Best Local Similarity
Matches 40; Conserv
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PEDULEM: DIDLING NEW COMMUNICATION OF THE PROPERTY OF THE PROPETTY OF THE PROPETTY OF THE PROP
Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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P49312; P97312,
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-UIL-2004 (Rel. 44, Last annotation update)
heterogeneous nuclear ribonucleoprotein Al (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein Al) (HDP-1) (Topoisomerase-inhibitor suppressed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93024387; PubMed=1406633;
Ben-David Y., Bani M.R., Chabot B., de Koven A., Bernstein A.;
"Retroviral insertions downstream of the heterogeneous nuclear ribonucleoprotein Al gene in erythroleukemia cells: evidence that Al is not essential for cell growth.";
Mol. Cell. Biol. 12:4449-4455(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lymphoma;

PUDDLINE=29766646; PubMed=8912629;

Onishi Y., Kizaki H.;

Onishi Z., Kizaki H.;

"Molecular cloning of the genes suppressed in RVC lymphoma cells by topoisomerase inhibitors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Hnrpal; Synonyms=Fli-2, Tis;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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0
                                                                                                                                                                                                                                                                                                                                               Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                 TISSUE=Pituitary gland,
Strausberg R.;
Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCG62235; AAH62235.1; -.
SEQUENCE 313 AA; 33620 MW; AE0EEC10972DEF7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 NOSSNFGPMKGGNFGGRSSGPYGGGGOYFAKPRNQGGYGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 40
                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                         'Match 93.8%; Score 228; DB 2; L
Local Similarity 100.0%; Pred. No. 2.2e-16;
les 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 228:7-13(1996).
                                                      and mouse cDNA sequences.
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its word modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REMEL; D86729; BAA13162.1; -
REMEL; D86729; BAA13162.1; -
REMEL; D86729; BAA13162.1; -
REMEL; AK007802; BAB25267.1; -
REMEL; AK088009; BAC40273.1; -
REMEL; A44485; A44485.
REMEL; A44485; A44485.
REMEL; A44485; A44485.
REMEL; AA4485; A44485.
REMEL; AA4485; A44485.
REMEL; AA4485; A44485.
REMEL; AA4485; AA4485.
REMEL; AA4485; AA4485.
REMEL; REME
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninoti P., Hayateu N., Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagwa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yashino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
Walli J., Yoshino M., Waterston R., Lander E.S., Rogers J., Burney E., Hawashizaki Y.;
Waterston R., Lander E.S., Rogers J., Mature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUDMED-SPHORYLATION SITES SER-5 AND SER-312.
Pubmed-14729942; DOI=10.1074/mcp.D300003-MCP200;
Shu H. Chen S., Bi Q., Mumby M., Brekken D.L.;
Shu H., Chen S., Bi Q., Mumby M., Brekken D.L.;
Identification of phosphoroteins and their phosphorylation sites in the WBHI-231 B lymphoma cell line.";
Mol. Cell. Proteomics 3:279-286(2004).
I- FUNCTION: Involved in the packaging of pre-mRNA into hnRNP
particles, transport of poly(A) mRNA from the nucleus to the cytoplasm and may modulate splice site selection.
SUBCELLULAR LOCATION: Nuclear. Shuttles continuously between the nucleus and the cytoplasm along with mRNA. Component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Short;
IsoId=P49312-2; Sequence=VSP_005825;
-!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asymmetric dimethylarginine (By
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/FTId=VSP 005825.
D80974FF2006B303 CRC64;
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Name=Long;
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193
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                     8. THE THE THE TRANSPERS TO THE TRANSPER
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cobianchi F., Karpel R.L., Williams K.R., Notario V., Wilson S.H., "Mammalian heterogeneous nuclear ribonucleoprotein complex protein Allarge-scale overproduction in Escherichia coli and cooperative binding to single-stranded nucleic acids."

J. Biol. Chem. 263:1063-1071(1988)

-!-FONGTION: Involved in the packaging of pre-mRNA into hnRNP particles, transport of poly(A) mRNA from the nucleus to the cytoplasm and may modulate splice site selection.

-!-SUBGELBULAR LOCATION: Nuclear. Shuttles continuously between the rubonucleosomes.
                                                                                                                                                                                                                                                                                                                                             Rattus norvėgicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
MEDINE=B66140140; PubMed=3005291;
Cobianchi F., Sengupta D.N., Zmudzka B.Z., Wilson S.H.;
"Structure of rodent helix-destabilizing protein revealed by CDNA
                                                                                                                                                                                                         20-WR-1987 (Rel. 04, Created)
01-WAR-1989 (Rel. 10, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Heterogeneous nuclear ribonucleoprotein Al (Helix-destabilizing protein) (AnnRNP core protein Al) (HDRNP).
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HSSP, P09651; 1UP1.
RGD, 69234; Hnrpal.
InterPro, IPRO0076; RRM 1; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50103; RRM; 1, 2.
PROSITE; PS0030; RRM; 1, 2.
Notet protein sequencing; Methylation; mRNA transport;
Nuclear protein; Phosphorylation; Repeat; Ribonucleoprotein;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cobianchi F.; Submitted (MAY-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                           267 NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 306
                                                                   40
                                                                     1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
93.8%; Score 228; DB 1; I 100.0%; Pred. No. 2.2e-16; ive 0; Mismatches 0;
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Globular B domain.
                                                                                                                                                                                            319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE.
MEDLINE=88087168; PubMed=2447078;
                                     Conservative
                                                                                                                                                                                              STANDARD;
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INIT MET 0
DOMAIN 3 93
DOMAIN 94 184
                  L Similarity
40; Conserv
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                                                                                                                                                                                                                                                                                                                                      Name=Hnrpal;
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   Query Match
Best Local S
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                    Best Loc
Matches
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us-09-763-982b-1.rup

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
B. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
B. Detchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M. J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
N. Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Helton B.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
B. Hakesley S.W., Touchman J.W., Green E.D., Dickson M.C.,
B. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
B. Rodiguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0
RNA-binding (RRM) 1.
RNA-binding (RRM) 2.
RNA-binding RGG-box.
Gly-rich.
NUCLEAR TARGETING SEQUENCE (BY SIMILARITY).
                                                                                                                                                                            Poly-Ser.
Phosphoserine (By similarity).
Asymmetric dimethylarginine.
Phosphoserine (By similarity).
E -> G (in Ref. 3).
W, C5BE7D183456B303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Submitted (UTN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: BC071945; AAH71945.1; -.
InterPro; IPR000504; RAM rec_mot.
Pfam; PF00076; RRM 1; 2.
RMART; SM00160; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50304; RRM: 2.
NUC1eccapsid; RIDDMJ RRM RNP 1; UNKNOWN 2.
NUC1eccapsid; Ribonucleoprotein.
SEQUENCE 320 AA; 34180 MW; 9069C6B40BDE1AF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Heterogeneous nuclear ribonucleoprotein Al, isoform a.
Name=HNRRA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 NQSSNFGPMKGGNFGGRSSGPYGGGGYFAKPRNQGGYGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
                                                                                                                                                                                                                                                                                                                                                                                 Score 228; DB 1; L
Pred. No. 2.2e-16;
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                                                                                                                                                                                                                                                                                                                                                                              93.8%; Score 228; DB ilarity 100.0%; Pred. No. 2.2 Conservative 0; Mismatches
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         96
183
239
319
304
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                                                                                                                                                                                                                                                                                                                        319 AA;
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es 40; Conserv
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TISSUE=Skin;
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         13
104
217
194
267
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MOD RES
MOD RES
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A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeoberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A papleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Tonshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brossk S.A., McKernan R.J., Malex J.A., Gunzarne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
M. Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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  Length 320;
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                                        Indels
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                                                                                                                                                                                                                              AAH12156;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Heterogeneous nuclear ribonucleoprotein Al, isoform a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH33714;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Heterogeneous nuclear ribonucleoprotein Al, isoform a.
                                                                                                                268 NOSSNFGPMKGGNFGGRSSGPYGGGGOYFAKPRNOGGYGG 307
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                                                                               1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
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93.8%; Score 228; DB 2; L
100.0%; Pred. No. 2.2e-16;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 40; Conservative 0; Mismatches 0;
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                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
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                    Best Local Similarity
Matches 40; Conserv
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ID AAH12158
      Query Match
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AAH33714
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Strausberg R.;
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                                                                                                                 MEDLINE=2238B257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Alusner R.D., Collins F.S., Wagner L., Shaefer C.F., Enat N.K.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Enat N.K.,
A Lischul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Enat N.K.,
A Lischul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Enat N.K.,
A Lischul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Datchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Schaefer M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Schards S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
A Nillalon D.K., Muxny D.M., Sodergren E.J., Lu X., Glibs R.A.,
A Villalon D.K., Muxny D.M., Madan A., Rodrigues S., Sanchez A.,
A Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Miting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Norley R.W., Tuckhman J.W., Green E.D., Dickson M.C.,
A Jones S.J., Marra M.A.,
A Jones S.J., Marra M.A.,
A Jones S.J., Marra M.A.,
A Generation and initial analysis of more than 15,000 full-length human
A mad mouse cDAR sequences."
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X MEDLINE=22388227; PubMed=12477932;

A Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

B tapleton M., Soares M.B., Bonaldo M.F., Caeavant T.L., Scheetz T.E.,

R the Brownstein M.J., Usdin T.B., Toshlytki S., Carninci P., Prange C.,

R Rhas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Rhey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 2.2e-16;
ive 0; Mismatches 0; Indels
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2002) to the EMBL; BC033714; AAH33714.1; Nucleocapsid; Ribonucleoprotein. SEQUENCE 320 AA; 34196 MW; 59485C9FAIFFBAEI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Heterogeneous nuclear ribonucleoprotein A1, isoform a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 NOSSNFGPMKGGNFGGFSSGPYGGGGQYFAKPRNQGGYGG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH02355 PRELIMINARY; PRT; AAH02355; Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Conservative
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Best Local Similarity
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                                                                             FROM N.A.
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                           NCBI TaxID=9606;
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AAH02355
AD AAH02355
AD AAH0
AC AAH0
DT 02-N
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TISSUB-BORD MARTOW;

MEDINE=2238827; PubMed=12477932;

MEDINE=2238827; PubMed=12477932;

MARIANE=2238827; PubMed=12477932;

MARIANE=238827; PubMed=12477932;

MARIANE=238827; PubMed=12477932;

MARIANE R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhata N.K.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

MARA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

MARA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

MARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MARA S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MARA S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MARIANG M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

MILING M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

MILING M., Touchman J.W., Green B.D., Dickson M.C., Shekin J.E.,

Ratywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

MARTA M.A.,

MARTA M.A.,

MARTA M.A.,

MARTA M.A.,

MAGHAR M., Schmutz J., Myers R.M., Butterfield Y.S.,

MARTA M.A.,

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MAGHAR M., Schmutz J., Myers R.M., Schein J.E.,

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MARTA M.A.,

MAGHAR M.,

MAGHA
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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100.0%; Pred. No. 2.2e-16;
tive 0; Mismatches 0; Indels
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EMBL, B2009600; AMP09600.1; -.
Nucleocapsid; Ribonucleoprotein.
SRQUENCE 320 AA; 34196 MW; S9485C9FA1FF8AEI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grausberg R.; Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC002355; AAH02255.1; -. Nucleoapsid; Ribonucleoprotein. s9485C9FA1FF8AE1 CRC64; APPRIENCE 320 AA; 34196 MM; 59485C9FA1FF8AE1
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02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Heterogeneous nuclear ribonucleoprotein Al, isoform a
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 2.2e-16;
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02-MAR-2004 (TrEMBLrel. 27, Created)
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Best Local Similarity 100.0
Matches 40; Conservative
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Best Local Similarity
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TISSUE=Liver;
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P09651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

A Sapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Sosak S.A., McEwan P.J., McKernn K.J., Malek J.A., Gunaratne P.H.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Holton E., Ketteman M., Roder A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rabakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Ratchiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human and manalysis of more than 15,000 full-length human
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL TaxID-9606;
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93.8%; Score 228; DB 2; Length 32
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 40; Conservative 0; Mismatches 0; Indels
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                             268 NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNOGGYGG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC070315; AAH70315.1; -.
SEQUENCE 320 AA; 34196 MW; 59485C9FA1FF8AE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH71945 PRELIMINARY, PRT, 320 AA.
AAH71945,
01-JUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
Heterogeneous nuclear ribonucleoprotein Al, isoform a.
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                                                                                                                                                                                                                         13-WAY-2004 (TrEMBLrel. 27, Created)
13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
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               1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG
                                                                                                                                                                                      320 AA
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                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                   HNRPA1 protein.
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ARESULT 11
ARH70315
DAH70315
DT 13-NG
DT 13-NG
DT 13-NG
DE HNRPP
GN HODE
RA ALAUR
RA ALAUR
RA ALAUR
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RASULE-SKINIS

RAS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ratausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Wokernan K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwam P.J., McKernan K.J., Malk J.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Radan A., Young A.C., Shevchenko Y., Boulfard G.G.,
RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodigutz A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RATWAINSKI M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE=88233978; PubMed=2836799;
Buvoli M., Blamonti G., Ghetti A., Riva S., Bassi M.T., Horandi C.;
"CDNA cloning of human hnRNP protein Al reveals the existence of multiple mRNA isoforms.",
Nucleic Acids Res. 16:3751-3770(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-AGG-1990 (Rel. 15, Last sequence update)
01-GCT-2004 (Rel. 45, Last annotation update)
Heterogeneous nuclear ribonucleoprotein Al (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein Al)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jasourner, Strausberg R.; Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC071345; AAH71245.1; -. Nucleocapsid; Ribonucleoprotein. SEQUENCE 320 AA; 34180 MW; 9069C6B408DE1AF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 NQSSNFGPMKGGNFGRSSGPYGGGGQYFAKPRNQGGYGG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002),
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100.0%; Pred. No. 2.2e-16;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 AA.
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Mol. Biol. 207:491-503(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Conservative
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SEQUENCE FROM N.A.
TISSUE=Skin;
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 MEDILNE-55286702; PubMed=7769000; Weighardt F., Biamonti G., Riva S.; Weighardt F., Biamonti G., Riva S.; "Nucleo-cytoplasmic distribution of human hnRNP proteins: a search for the targeting domains in hnRNP Al."; Ucell Sci. 108:545-555(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shamoo Y., Krueger U., Rice L.M., Williams K.R., Steitz T.A.;
"Crystal structure of the two RNA binding domains of human hnRNP A1 at 1.75-A resolution.";
Nat. Struct. Biol. 4:215-222(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE 97277240; PubMed=9115444;
Xu R.W., Okhan L., Cheng X., Mayeda A., Krainer A.R.;
Kur R.W., Okhan L., Cheng X., Mayeda A., Krainer A.R.;
Kur Crystal structure of human UP1, the domain of hnRNP A1 that contains
two RNA-recognition motifs.";
Structure 5:559-570(11997).
-1- FUNCTION: Involved in the packaging of pre-mRNA into hnRNP
particles, transport of poly(A) mRNA from the nucleus to the
cytoplasm and may modulate splice site selection.
-1- SUBCELLULAR LOCATION: Nuclear. Shuttles continuously between the
nucleus and the cytoplasm along with mRNA. Component of
                                                                                                                                                                                                                                                                                                                                                                         NUCLEAR LOCALIZATION DOMAIN, AND NUCLEAR EXPORT.
MEDLINE=96067639; PubMed=8521471;
Michael W.M., Choi M., Dreyfuss G.;
"A nuclear export signal in hnRNP Al: a signal-mediated, temperature-dependent nuclear protein export pathway.";
(cell 83:415-422(1995).
                                                                       TISSUB-Liver;
MEDILINE-87053868; PubMed=3023065;
Riva S., Morandi C., Tsoulfas P., Pandolfo M., Biamonti G.,
Merrill B., Williams K.R., Multhaup G., Beyreuther K., Werr H.,
Heinrich B., Schaefer K.P.; Multhaup G., Beyreuther K., Werr H.,
Mammanlan single-stranded DNA binding protein UP I is derived from the hnRNP core protein Al.";
EMBO J. 5:2267-2273(1986).
                                                                                                                                                                                                   MEDLINE $90214633; PubMed=1691095;
Buvoli M., Cobianchi F., Bestagno M.G., Mangiarotti A., Bassi M.T.,
Blamonti G., Riva S.;
"Alternative splicing in the human gene for the core protein Al
generates another hnRNP protein.";
EMBO J. 9:1229-1235(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D-STRUCTURE MODELING OF 106-189.
MEDLINE=31099515; PubMed=2176620;
Metheri A., Bolognesi M., Cobianchi F., Morandi C.;
"Modeling by homology of RNA binding domain in Al hnRNP protein.";
FEBS Lett. 277:272-276(1990).
                                                                                                                                                                                                                                                                                                                        Siomi H., Dreyfuss G., "A nuclear localization domain in the hnRNP Al protein."; J. Cell Biol. 129:551-560(1995).
        TISSUB=Lung,
Knudsen S.M., Leffers H.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.75 ANGSTROMS) OF 8-180.
MEDLINE=97307256; PubMed=9164463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 6-181.
                                                                                                                                                                                           SEQUENCE OF 251-302 FROM N.A. (ISOFORM A1-B).
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IsoId=P09651-1; Sequence=Displayed;
SEQUENCE FROM N.A. (ISOFORM A1-A)
                                                                                                                                                                                                                                                                                                NUCLEAR LOCALIZATION DOMAIN, MEDLINE=95247808; Pubmed=7730395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION DOMAIN.
                                                             PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=A1-A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
Phosphosetine (By similarity).
Missing (in isoform Al-A).
/FIId=VSP 005824.
N >> 8 (in dbSNP 6533).
/FIId=VAR 014711.
G->A: No nuclear import nor export.
G->A: No nuclear import nor export.
GG->Li. Normal nuclear import and export.
R >> P (in Ref. 4).
IsoId=P09651-2; Sequence=VSP_005824;
Note=Is twenty times more abundant than isoform A1-B;
-!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR TARGETING SEQUENCE (M9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphoserine (By similarity). Asymmetric dimethylarginine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Globular A domain.
Globular B domain.
RNA-binding (RRM) 1.
RNA-binding (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding RGG-box.
                                                                                                                                                                                                                                                                                                                                   Aarhus/Ghent-2DPAGE; 207; NEPHGE.
Aarhus/Ghent-2DPAGE; 2114; NEPHGE.
Aarhus/Ghent-2DPAGE; 3612; NEPHGE.
                                                                                                                                                         EMBL; X12671; CAA31191.1; -.
BEBL; X06747; CAA52922.1; ALT_SEQ.
EMBL; X04347; CAA27374.1; -.
EMBL; X79536; CAA56072.1; -.
                                                                                                                                                                                                           PIR, S02061, S02061.
PDB; 1HA1; X-ray; @=1-183.
PDB; 1D3K, X-ray; @=1-195.
PDB; 1PG2; X-ray; A=1-195.
PDB; 1PO6; X-ray; A=7-189.
PDB; UVP1; X-ray; A=7-189.
INCACT; P09651; --
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Reactome, P09651; -.
MIM; 164017;
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184
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SWISS-2DPAGE;
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VARSPLIC
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CONFLICT
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Name-bA438F9.2;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 9.6e-16;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                       Phosphoserine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
BA438F9.2 (Novel protein similar to heterogeneous nuclear ribonucleoprotein A1 (HNRPAI)) (Fragment).
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 219; DB 2; Lengtn /v
Pred. No. 4.7e-16;
"......hhes 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bates K.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                  5A04D9E3BFD969E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              267 NOSSNFGPMKGGNFGGRSLGPYGGGGQYFAKPRNQGGYGG 306
                                                                                                                                                                                                                                                                                                                                                      1 NOSSNFGPMKGGNFGGRSSGPYGGGGGYFAKPRNQGGYGG 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AL390738; CAC12722.1; -. GO: GO:0030529; C:ribonucleoprotein complex; IEAGO: GO:0019013; C:viral nucleocapsid; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
90.1%; Score 219; DB
Best Local Similarity 97.5%; Pred. No. 4.7e
Matches 39; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: October 22, 2004, 13:46:24 Job time : 197 secs
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      PROSITE, PSS0102; RR
PROSITE; PS00030; RR
Methylation; mRNA tr
Ribonucleoprotein; R
INIT MET 3
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307 3
319 AA;
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Best Local Similarity
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193
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SEQUENCE
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Q9H4S1;
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Q9H4S1
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Heterogeneous nuclear ribonucleoprotein Al (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein Al)
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                                                                                                                                                                                                                                                                                    93.8%; Score 228; DB 1; Length 371; 100.0%; Pred. No. 2.5e-16; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                          38715 MW; B3EEFA5AE1DB7C26 CRC64;
                                                                                                                                                                                                                                                                                                                                                             319 NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 358
                                                                                                                                                                                                                                                                                                                                              1 NOSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 AA
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TISSUB-Tracheobronchial epithelium;
MEDLINE-93192320; PubMed-8448206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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 73
880
880
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887
871
1127
1127
1152
1165
1169
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Thes 40; Conserve
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ROA1 MACMU Q28521;

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NCBI\_TaxID=9544;

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Gaps

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Gaps

188P; P09651; 2UP1. InterPro; IPR000504; RNA\_rec\_mot. Pfam; PF00076; RRM\_1; 2.

Pfam;

EMBL; M84334; AAB01436.1; -.

\$30192; \$30192.